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Assessment of Biofilm Formation Potential among Multiple Drug Resistant *Escherichia coli* Strains with Potential to Produce Shiga Toxins Isolated from Various Chicken Meats

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ABSTRACT

Escherichia coli **is an important bacterial pathogen capable of multiple drug resistance and biofilm formation. Its presence in meats and their products may eventually lead to outbreaks especially if the pathogenic multidrug resistant strains are involved. The aim of this study was to determine the presence of *Escherichia coli* isolated from chicken meat samples in Gombe metropolis, their multidrug resistance as well as their potential to produce biofilms. A total of 60 chicken parts; 10 samples from each of chicken breast, drumstick, wings, thighs, backs and legs were purchased and analyzed. Specimens were immediately transferred to the laboratory in a cooler with an ice pack. The bacteriological culture-based technique on Eosin Methylene Blue (EMB) agar and Gram staining and further phenotypic identification techniques were employed to characterize the organism. Antimicrobial susceptibility testing using agar-disc diffusion was performed with 10 commonly used antibiotics using Mueller-Hinton agar. The incidence of *E. coli* was highest in the chicken legs with 33.3% (n= 10) and lowest in drumstick with 6.7% (n=02). The highest contamination level of *E. coli* was in chicken legs with 3.00 x 10^3 CFU/g while the lowest was observed in drumstick at 1.32 x 10^3 CFU/g. There was high resistance to Amoxycillin (100%), Tetracycline (100%), Doxycycline (93.3%), Mecillinam (90%) and Levofloxacin (70%). There was low resistance to Ciprofloxacin (10%), Streptomycin (10%), Ceftazidime (13.3%) and Ceftriaxone (16.7%). All the isolates except WEC 3 and LEC 10 were multidrug resistant. The multiple antibiotic resistance index (MARI) ranged from 0.3 to 0.7 indicating high risk of disease and eventually if not checked, can lead to outbreaks.**

1.0 INTRODUCTION

Chicken meat is considered the most widely consumed meat globally. It has been reported that there are almost 19 billion chickens in the world. This makes it the commonest birds' species (Mpundu et al., 2019). A data revealed by Uzundumlu and Dilli (2022) showed that there was 118 million tons of poultry produced worldwide.

However, due to lack strict hygiene practices operation in the primary and secondary production lines as well as the final product of the food chain, bacteria particularly those of public health importance contaminate the chicken and its products. These include *Salmonella spp*. and coliforms especially *Escherichia coli* which is among the normal microbial flora of gastrointestinal tracts of various animals including chickens and man. These bacteria are the global lead causes of foodborne ailments including gastroenteritis. It is a major global cause of chronic and acute foodborne diseases in humans and poultry (Mpundu et al., 2019).

E. coli is a bacterium that inhabits the intestines of both man and animals and its presence indicates faecal contamination that usually arises from contamination by human faeces via water or food source. *E. coli* in chicken meat is an indicator of poor hygiene practices in places where the chickens are slaughtered, processed or vended. In addition, *E. coli* was found to be prevalent in various parts of the world such as in India with 98% prevalence (Sharma and Chattopadhyay, 2015), In Pakistan, with 43.5% prevalence (Zainab et al., 2022) in Morocco with 48.4% (Cohen et al., 2020) in Nigeria with prevalence of 99.4% (Agusi et al., 2024) and 82.3% in Malaysia (Suryadevara et al., 2020).

The above findings for the contamination of *E. coli* in chickens from different countries around the globe are reflections of varying hygiene practices and quality controls. Those recording lower contamination levels are believed to have better hygiene and manufacturing practices in their processes of slaughter. The high contamination is an indication that meat from chicken is a important public health issue with the potential for causing foodborne infections and intoxications in humans that may consequently lead to outbreaks due to the organisms involved (Mpundu et al., 2019). Due to various food consumption patterns including consumption of chicken meat, globally people suffer from foodborne ailments throughout the year. Thus, reducing the levels of contamination at various stages of processing can significantly impact the reduction of incidences associated with consumption of contaminated poultry meats and their products (Keener et al., 2004; Adu-Gyamfi et al., 2012).

Antibiotics in large quantities have been employed to treat or prevent occurrence of diseases. They are also used to promote growth in the production of poultry (Allen et al., 2013). This leads to an indiscriminate antibiotic use in the course of poultry production. For this purpose also, almost all antibiotics employed have been utilized in human medicine, most at times not for therapy but for prevention. Consequently, there is an increase in the emergence of antibiotic resistant bacterial pathogens that are associated with diseases (Rafiq et al., 2024). This is an issue for concern as there is also the growth of antibiotic resistance gene pool in commensal bacteria. Thus there is need for intensive research to understand the growing dynamics as well as the prevalence of antibiotic resistant bacteria in poultry meats and their products (Roth et al., 2019).

2.0 MATERIALS AND METHODS

2.1 Sampling and Sample Processing

A total of 60 samples, 10 from each of the chicken breast, drumstick, wings, thighs, backs and legs were purchased from vendors viz; Pasar Malam (night market), Pasar Borong, Pasaraya Borong and Hero Mart in Sri Serdang, Selangor Malaysia. The samples were obtained in six visits to each vendor for nine months; from July, 2016 to March, 2017. The samples were aseptically placed immediately after purchase in sterile plastic bag and transported to the laboratory at the Center of Excellence for Food Safety Research, Faculty of Food Science and Technology, Universiti Putra Malaysia, within two hours for analysis.

2.2 Isolation, Identification and Enumeration of Coliforms and *E. coli*

The microbial analysis was carried out to determine the prevalence of coliforms and *E. coli* in the chicken meats. A 25 g of each of the samples was aseptically cut into smaller pieces using a sterile knife. They were then macerated and homogenized with 225 mL of sterile buffered peptone water in a stomacher bag using stomacher. Following homogenization, the samples were serially diluted into 10^{-1}, 10^{-2}, and 10^{-3} dilutions. To determine the bacteria growth, 0.1 mL from each dilutions series was spread onto MacConkey agar (MA) and Eosin Methylene Blue (EMB) agar and incubated in an incubator for 24 hours at 37°C. The colony forming unit per gram (CFU/g) was counted after the incubation.

2.3 Phenotypic Identification of Coliforms and *E. coli*

Isolates presumably identified as coliforms on MA and *E. coli* on EMB agar were further subjected to gram staining and biochemical tests such as indole production, citrate utilization, urease, ornithine decarboxylase, motility, hydrogen sulphide, gas and acid production, Voges-Proskauer and methyl red. They were identified as members of the coliforms, non-coliform members or *E. coli* in particular.

2.6 Antibiotic Susceptibility Testing

The antibiotic susceptibility testing on the isolated *E. coli* was conducted against 10 common antibiotics; ciprofloxacin, Levofloxacin, Gentamicin, Streptomycin, Ceftriaxone, Ceftazidime, Mecillinam, Amoxycillin, Tetracycline and Doxycycline. Agar-disk diffusion technique on Mueller-Hinton agar (MHA) was the procedure employed following the standardization of the inoculum that matched with the 0.5 McFarland turbidity standard equivalent of 1.5×10^8 CFU/mL. Standard antibiotic discs were dispensed and the medium incubated at 37 °C for 24 hours at an inverted position. Zones of inhibition were recorded following incubation and the results were interpreted in accordance with Clinical and Laboratory Standard Institute (CLSI, 2024). Each isolate was interpreted based on its response against the tested antibiotic as “Resistant, Intermediate or Sensitive.”

2.7 Multidrug Resistance Determination

The determination of multidrug resistance (MDR) was done based on the definition that MDR is the resistance by an organism to at least one antibiotic from three or more different antibiotic classes. An organism resistant to many antibiotics from one or two classes is not regarded a multidrug resistant organism.

2.8 Determination of Biofilm Formation Potential

The 28 multidrug resistant *S. aureus* strains were subcultured on TSB and subjected to incubation at 37°C for one day. Following incubation, the subcultured organisms were also subjected to dilution in a ratio of 1:100 in TSB of 0.25% glucose supplement. Aliquot of 200 ml of all the dilutions was dispensed into each well of plastic 96-well microtitre plate (SPL, Life Science, Korea) and the organisms in the plate were subjected to incubation for one day at 37°C.

After incubation, the wells were washed 3 times with PBS (pH 7.4±0.1; Thermo Fisher Scientific, Waltham, Massachusetts, USA), air-dried for 1 h at 60°C. The dried wells were stained with 0.25% crystal violet and incubated at room temperature for 15 min. The absorbance at OD_{570nm} was determined after washing. The mean absorbance of each test well was classified according to Stepanovic et al. (2000) as non-biofilm former, weak, moderate or strong biofilm formers relative to the control and uninoculated wells of the plate. The non-biofilm formers were the ones with absorbance less than or equal to the control wells ($OD \leq OD_C$); the weak biofilm formers ($OD_C \leq OD \leq 2x\ OD_C$), moderate biofilm formers ($2x\ OD_C \leq OD \leq 4x\ OD_C$) and the strong biofilm formers ($4x\ OD_C < OD$). All the isolates were used for the formation of biofilms in this assay in quadruplicate. Finally, the mean absorbance was calculated. The analyses were repeated separately in three separate occasions (O'Toole, 2011). The ATCC *S. epidermidis* (ATCC 35983) and *S. epidermidis* (ATCC 12228) were respectively used as positive and negative controls to assess the strains BFP.

3.0 RESULTS

A total of 10 samples were collected from each of chicken breast, drumstick, chicken wings, thigh, back and legs. Out of the 10 samples of chicken breast collected, only 04 (40%) samples were positive for *E. coli*, 02 accounting for 20% for *K. pneumoniae*, 01 accounting for 10% for the presence of *Citrobacter spp.* and no sample was found to harbour *E. aerogenes* (Table 3.1). Meanwhile, out of the 10 samples from drumstick, only 02 (20%) and 01(10%) samples were positive for *E. coli* and *K.*

pneumoniae respectively. *Citrobacter spp.* and *E. aerogenes* were not found at all. In addition, 05, 02, 01 and 01 accounting for 50%, 20%, 10% and 10% of the samples from chicken wings were found to be positive for *E. coli, K. pneumoniae, Citrobacter spp.* and *E. aerogenes* respectively. However, of the 10 samples from chicken thigh, 05 (50%), 03(30%), 02 (20%) and 01(10%) were found to harbour *E. coli, K. pneumoniae, Citrobacter spp.* and *E. aerogenes* respectively. In chicken backs, only 04 (40%) and 02 (20%) were positive for *E. coli, K. pneumoniae* respectively wherein *Citrobacter spp.* and *E. aerogenes* were absent. In the chicken legs samples, all the 10 samples (100%) were positive for *E. coli*, half of the samples (50%) were positive for *K. pneumoniae*, 02 (20%) samples harboured *Citrobacter sp.* and 02 (20%) were positive for *E. aerogenes*.

Table 3.1: Prevalence of coliform bacteria from poultry meat samples based on culture and staining properties

Meat type	No. of Samples	*E. coli* No. (%)	*K. pneumoniae* No. (%)	*Citrobacter sp.* No. (%)	*E. aerogenes* No. (%)
Chicken breast	10	04 (40)	02 (20)	01 (10)	00 (00)
Drumstick	10	02 (20)	01 (10)	00 (00)	00 (00)
Chicken wings	10	05 (50)	02 (20)	01 (10)	01 (10)
Chicken thighs	10	05 (50)	03 (30)	02 (20)	01 (10)
Chicken backs	10	04 (40)	02 (20)	00 (00)	00 (00)
Chicken legs	10	10 (10)	05 (50)	02 (20)	02 (20)
Total	**60**	**30**	**16**	**06**	**04**

It can be observed that the values of the *E. coli* count that determines the contamination rate are in multiples of x 10^3 CFU/g of the sample. The chicken breast had 2.52, 2.12, 2.11 and 2.61 x 10^3 CFU/g for samples CBEC 1, CBEC 2, CBEC 3 and CBEC 4 respectively. Meanwhile, DEC 1 and DEC 2 from drumstick had 1.50 and 1.32 x 10^3 CFU/g (Table 3.2).

Table 3.2: Determination of total *E. coli* count and the prevalence of shiga toxin from poultry meat types

S/N	Sample Identity	Total *E. coli* Count (x 10^3 CFU/g)	Poultry Meat Type
1	CBEC 1	2.52	Chicken breast
2	CBEC 2	2.12	Chicken breast
3	CBEC 3	2.11	Chicken breast
4	CBEC 4	2.61	Chicken breast
5	DEC 1	1.50	Drumstick
6	DEC 2	1.32	Drumstick
7	WEC 1	2.80	Wings
8	WEC 2	2.65	Wings
9	WEC 3	2.11	Wings
10	WEC 4	2.12	Wings
11	WEC 5	2.62	Wings
12	TEC 1	2.00	Thighs
13	TEC 2	2.00	Thighs
14	TEC 3	2.61	Thighs
15	TEC 4	2.23	Thighs
16	TEC 5	2.25	Thighs
17	BEC 1	2.22	Back
18	BEC 2	2.32	Back
19	BEC 3	2.63	Back
20	BEC 4	2.80	Back
21	LEC 1	2.52	Legs
22	LEC 2	2.24	Legs
23	LEC 3	2.52	Legs
24	LEC 4	2.70	Legs
25	LEC 5	2.21	Legs
26	LEC 6	2.20	Legs
27	LEC 7	2.50	Legs
28	LEC 8	2.80	Legs
29	LEC 9	3.00	Legs
30	LEC 10	2.20	Legs

Key: - = negative, + = positive

The five samples from wings as WEC 1, WEC 2, WEC 3, WEC 4 and WEC 5 had counts of 2.80, 2.65, 2.11, 2.12 and 2.62 x 10^3 CFU/g respectively. Samples from chicken thighs had values of *E. coli* counts of 2.00, 2.00, 2.61, 2.23 and 2.25 x 10^3 CFU/g for TEC 1, TEC 2, TEC 3, TEC 4 and TEC 5 respectively. The chicken back samples viz; BEC 1, BEC 2, BEC 3 and BEC 4 had 2.22, 2.32, 2.63 and 2.80 x 10^3 CFU/g colony counts respectively. For the chicken leg samples LEC 1, LEC 2, LEC 3, LEC 4, LEC 5, LEC 6, LEC 7, LEC 8, LEC 9, and LEC 10, the *E. coli* colony counts were 2.52, 2.24, 2.52, 2.70, 2.21, 2.20, 2.50, 2.80, 3.00 and 2.20 respectively.

The antimicrobial resistance of the 30 *E. coli* strains isolated from the cutting boards of some selected households in Gombe metropolis is depicted in Table 3.3. Out of the 30 isolates, only 10% (n=3) were resistant to Ciprofloxacin, 70% (n=21) to Levofloxacin, 30% (n=9) were resistant to Gentamicin, 10% (n=3) to streptomycin, 16.7% (n=5) to Ceftriaxone, 13.3% (n=4) to Ceftazidime, 90% (n=27) to Mecillinam and 100% (n=30) to Amoxycillin. Additionally, 100% (n=30) were found to be resistant to Tetracycline and 93.3% (n=28) to Doxycycline. There was no susceptible isolate to Mecillinam, Amoxycillin, Tetracycline and Doxycycline.

Table 3.3: Antimicrobial sensitivity of *E. coli* (n=30) isolated from cutting boards of some selected households against commonly used antibiotics

Antibiotics (Conc.)	Resistant		Intermediate		Susceptible	
	Positive strain n(%)	Zone diameter (mm)	Positive strain n(%)	Zone diameter (mm)	Positive strain n(%)	Zone diameter (mm)
Ciprofloxacin(10µg)	03(10)	≤21	00(00)	22-25	27 (90)	≥26
Levofloxacin(10µg)	21(70)	≤16	06(20)	17-20	03(10)	≥21
Gentamicin (10µg)	09(30)	≤14	00(00)	15-17	21(70)	≥18
Streptomycin(10µg)	03(10)	≤11	03(10)	12-14	24(80)	≥15
Ceftriaxone(30µg)	05(16.7)	≤22	07(23.3)	23-25	18(60)	≥26
Ceftazidime(30µg)	04(13.3)	≤17	06(20)	18-20	20(66.7)	≥21
Mecillinam(10µg)	27(90)	≤11	03(10)	12-14	00(00)	≥15
Amoxycillin(10µg)	30(100)	≤13	00(00)	14-16	00(00)	≥17
Tetracycline(30µg)	30(100)	≤11	00(00)	12-14	00(00)	≥15
Doxycycline(30µg)	28(93.3)	≤10	02(6.7)	11-13	00(00)	≥14

Additionally, Table 3.4 displays the multiple antibiotic resistance (MAR) patterns of the 30 isolated *E. coli* strains showing each of the strain the number of antibiotics to which it was resistant. This is also accompanied in parentheses the total number of the groups to which that strain was resistant. This is used to determine whether a strain is multidrug resistant (MDR) or non- multidrug resistant (non-MDR). A strain is said to be multidrug resistant if it is resistant to at least one antibiotic from three different classes of antibiotic classes. It can be observed that CBEC 1 and CBEC 2 were resistant to seven antibiotics each and although the antibiotics may differ to a little extent, those to which CBEC 1 was resistant are from five different classes while those to which CBEC 2 was resistant are from four different antibiotic classes. Others such as CBEC 3, WEC 1, WEC 4, BEC 3, LEC 4, LEC 5 and LEC 8 were resistant to six antibiotics belonging to four different classes. However, strain DEC 1 was resistant to six antibiotics but from three different classes. CBEC 4, DEC 2, WEC 2, WEC 5, TEC 1, TEC 2, TEC 4, BEC 1, BEC 2, BEC 4, LEC 2, LEC 6, LEC 7 and LEC 9 were each resistant to five antibiotics from three different classes except LEC 9 in which the antibiotics are from four different classes. Moreover, strains such as TEC 3, LEC 1, LEC 3 and WEC 3 were found to be resistant to four different antibiotics from three different classes except WEC 3 in which the antibiotics are from two different classes; and therefore is non-MDR. Isolate LEC 10 was resistant to only three antibiotics from two different classes and thus is also non-MDR. Lastly, strain with the identity TEC 5 was the one with highest number of resistant being resistant to nine different antibiotics. However, these antibiotics are from five different antibiotic classes.

The multiple antibiotic resistance index (MARI) is the measure of a ratio of the number of antibiotics to which an organism is resistant to the total number of antibiotics to which the organism is exposed, mathematically represented as;

MARI = TAR/TAU

Where TAR is the total antibiotic resistant; and TAU is total antibiotic used. It can be observed that all the *E. coli* strains have the MARIs that range from 0.3 to 0.7.

Table 3.4: Antibiotic resistance profile and multiple antibiotic resistance index of individual E. coli isolated from cutting boards of some selected households

Isolate	Antibiotic resistant profile*	No. of antibiotics**	MAR Index***
CBEC 1	LEV GEN CRO MEC AMX TCN DCN	**7 (5)**	0.7
CBEC 2	CIP LEV CAZ MEC AMX TCN DCN	**7 (4)**	0.7
CBEC 3	LEV CRO MEC AMX TCN DCN	**6 (4)**	0.6
CBEC 4	LEV MEC AMX TCN DCN	**5 (3)**	0.5
DEC 1	CIP LEV MEC AMX TCN DCN	**6 (3)**	0.6
DEC 2	GEN MEC AMX TCN DCN	**5 (3)**	0.5
WEC 1	LEV GEN MEC AMX TCN DCN	**6 (4)**	0.6
WEC 2	LEV MEC AMX TCN DCN	**5 (3)**	0.5
WEC 3	MEC AMX TCN DCN	**4 (2)**	0.4
WEC 4	LEV GEN S AMX TCN DCN	**6 (4)**	0.6
WEC 5	LEV MEC AMX TCN DCN	**5 (3)**	0.5
TEC 1	LEV MEC AMX TCN DCN	**5 (3)**	0.5
TEC 2	LEV MEC AMX TCN DCN	**5 (3)**	0.5
TEC 3	GEN AMX TCN DCN	**4 (3)**	0.4
TEC 4	LEV MEC AMX TCN DCN	**5 (3)**	0.5
TEC 5	CIP LEV GEN S CRO MEC AMX TCN DCN	**9 (5)**	0.9
BEC 1	CAZ MEC AMX TCN DCN	**5 (3)**	0.5
BEC 2	LEV MEC AMX TCN DCN	**5 (3)**	0.5
BEC 3	LEV CAZ MEC AMX TCN DCN	**6 (4)**	0.6
BEC 4	LEV MEC AMX TCN DCN	**5 (3)**	0.5
LEC 1	MEC AMX TCN DCN	**4 (3)**	0.4
LEC 2	LEV MEC AMX TCN DCN	**5 (3)**	0.5
LEC 3	LEV MEC AMX TCN	**4 (3)**	0.4
LEC 4	LEV GEN MEC AMX TCN DCN	**6 (4)**	0.6
LEC 5	LEV CTR MEC AMX TCN DCN	**6 (4)**	0.6
LEC 6	LEV MEC AMX TCN DCN	**5 (3)**	0.5
LEC 7	CAZ MEC AMX TCN DCN	**5 (3)**	0.5
LEC 8	GEN S CTR AMX TCN DCN	**6 (4)**	0.6
LEC 9	LEV GEN AMX TCN DCN	**5 (4)**	0.5
LEC 10	MEC AMX TCN	**3 (2)**	0.3

***** CIP=Ciprofloxacin, LEV=Levofloxacin, AMX=Amoxycillin, GEN=Gentamicin, MEC=Mecillinam CRO=Ceftriaxone, TCN=Tetracycline, S=Streptomycin, CAZ=Ceftazidime, DCN=Doxycycline.

**The number of antibiotics to which each isolate was resistant. The number in the parenthesis indicates the total number of the classes the antibiotics belong.

DISCUSSION

Meats from poultry are vital components of diets in humans. This is owing to the presence of protein, mineral and vitamins. However, those meats are prone to contamination by bacterial pathogens that cause food poisoning (Zainab et al., 2022).

The results obtained from the prevalence of coliforms in poultry meat from various parts showed highest occurrence (100%) of *E. coli*. This is because this organism is the most prevalent bacterial strain on earth as well as a model organism for biotechnological research. It is equally the simplest bacterium that serves as indicator for faecal contamination. This in turn indicates poor hygiene practice whenever they are found to be associated with poultry meats (Mpundu et al., 2019). The high numbers of coliforms particularly *E. coli* and *K. pneumoniae* in the poultry meats represent a potential source for human colonization and infection as well as spread within the community (Eibach et al., 2018). The presence of other coliforms (*Citrobacter sp.* and *E. aerogenes*) in the poultry meat samples analyzed is akin to the presence of *E. coli* and *K. pneumoniae* and is an indication of poor hygiene practice as well as improper handling of the meats (Mukesh et al., 2018). Higher prevalence of *E. coli* was found in chicken legs. This may be attributed to the fact that legs are the first contact of the poultry to the ground where faeces are found. Additionally, the scaly nature of the legs and the uneasy nature of the scale removal and cleaning may another contributing factor. The lowest prevalence was observed in drumstick as that is the part of chicken meat that can be cleaned more easily than the other parts. This contradicts the findings of Enver et al. (2021) in which the drumstick had the highest prevalence of *E. coli* (4.75 x 10^3 CFU/g) as against the chest, wing and offal.

Prior to consumption, meat from poultry should be absolutely free from *E. coli* due to the severity and

nature of the infection or intoxication induced by the bacterium in humans (Ishola and Taiwo, 2014). For the screening of foodborne pathogens, *E. coli* is frequently employed as an indicator of safety for microbiological importance (Foddai and Grant, 2020). In this research, the rate of isolation of *E. coli* was 50.0 %; closely related to that obtained by Rafiq et al. (2024) and lower than 63.5 % rate of detection by Rahman et al.(2020).

In this study, the *E. coli* count indicates that the isolated strains were not within the acceptable limit (≤100 CFU/g) as per as the International Commission on Microbiological Specifications of food (ICMSF) specifications for the total coliform count is concerned. This indicates a threat of infections due to *E*. *coli* (Loo et al., 2013) and consequently outbreaks (Mpundu et al., 2019). The figures obtained in this study with regard to the *E. coli* and other coliform bacteria is much more than the acceptable limit (>2000 CFU/g). Similar results were obtained by Hassanien et al. (2015), Kim et al. (2018) and Enver et al. (2021). The coliform counts and in particular, *E. coli* counts increase during the course processing to the final products from raw materials (Kim et al., 2018).

Antibiotic resistance of *E. coli* to Penicillin family has not been uncommon as Tan et al. (2014) recorded 85.71% in which herein 100% and 93% were resistant to Amoxycillin and Mecillinam respectively. The reason may be that these antibiotics exhibit their antimicrobial activity more on Gram positive bacteria than on their Gram negative bacteria by inhibition of peptidoglycan layer. This peptidoglycan layer accounts for the 90% of the Gram positive bacterial cell wall. A high percentage of resistance to Tetracycline and Doxycycline has also been reported by Tan et al. (2014) and Akond et al. (2009). Resistance to antibiotics used in this study has been consistent with those obtained by Melo et al. (2015) Susceptibility to Ciprofloxacin was high as reported in this study but was low against Norfloxacin although from the same antibiotic class (fluoroquinolones)

The Multiple Antibiotic Resistance Index (MARI) displayed in Table 3.4 represents a vital analysis for checking the risk factors associated with resistance to antibiotics. MARI is determined from the ratio of sum of antibiotics the strain resisted to that of the antibiotics against which the strain was tested. Bacterial strains that have MARI ≥ 0.2 indicate that their origin is high-risk sources of contaminations; areas where various antibiotics have been utilized (Sandhu et al., 2016; Afunwa et al., 2020).

Bacterial strains having MARI values of ≥0.2 can lead to the presence of multidrug resistance genes that originate from environments where there is incessant abuse of such drugs. This also indicates that there is a plasmid harbouring one or more genes that encode for phenotypic resistance to antibiotic class or some members of same class. The use of MARI analysis is not a method that requires special training, nor does it require equipment that are costly to obtain (Ejiofor et al., 2016; Afunwa et al., 2020).

CONCLUSION

Poultry meat types were screened for the presence of coliforms and *E. coli* in particular. All samples obtained from the chicken legs were positive for *E. coli*. In addition, high *E. coli* count was observed in samples from chicken legs and the lowest from drumstick. Poor personal hygiene that may lead to transfer of coliform bacteria and *E. coli* as well as improper handling and processing of the poultry meats may be the main contributing factors toward the prevalence of the pathogenic bacteria. a strain that is great threat and risk to the health of the consumers and the public as a whole. This can bring in addition to the rise in mortality rate great economic loss.
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CONFLICT OF INTEREST

There was no conflict of interest among the authors of this research.

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